

## **IN THE SPECIFICATION**

Page 14, replace the paragraph starting on line 11 with the following:

The skilled person will be aware of the fact that several different computer programmes are available to determine the homology between two sequences. For instance, a comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. In a preferred embodiment, the percent identity between two amino acid sequences is determined using the Needleman and Wunsch (J. Mol. Biol. (48): 444-453 (1970)) algorithm which has been incorporated into the GAP program in the GCG software package (available at [www dot gcg dot com](http://www.gcg.com) ~~http://www.gcg.com~~), using either a Blossom 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. The skilled person will appreciate that all these different parameters will yield slightly different results but that the overall percentage identity of two sequences is not significantly altered when using different algorithms.

Page 14, replace the paragraph starting on line 23 with the following:

In yet another embodiment, the percent identity between two nucleotide sequences is determined using the GAP program in the GCG software package (available at [www dot gcg dot com](http://www.gcg.com) ~~http://www.gcg.com~~), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. In another embodiment, the percent identity two amino acid or nucleotide sequence is determined using the algorithm of E. Meyers and W. Miller (CABIOS, 4:11-17 (1989)) which has been incorporated into the ALIGN program (version 2.0) (available at: [vega dot igh dot cnrs dot fr slash bin slash align-guess dot cgi](http://vega.igh.cnrs.fr/bin/align-guess.cgi) ~~http://vega.igh.cnrs.fr/bin/align-guess.cgi~~) using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4.

Page 14, replace the paragraph starting on line 32 with the following:

The nucleic acid and protein sequences of the present invention can further be used as a "query sequence" to perform a search against public databases to, for

example, identify other family members or related sequences. Such searches can be performed using the BLASTN and BLASTX programs (version 2.0) of Altschul, et al. (1990) J. Mol. Biol. 215:403-10. BLAST nucleotide searches can be performed with the BLASTN program, score = 100, word length = 12 to obtain nucleotide sequences homologous to PLP03 nucleic acid molecules of the invention. BLAST protein searches can be performed with the BLASTX program, score = 50, word length = 3 to obtain amino acid sequences homologous to PLP03 protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al., (1997) Nucleic Acids Res. 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., BLASTX and BLASTN) can be used. See [www dot ncbi dot nlm dot nih dot gov](http://www.ncbi.nlm.nih.gov) <http://www.ncbi.nlm.nih.gov>.